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OIPE

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/809,638

DATE: 08/08/2001  
 TIME: 11:01:34

Input Set : A:\Seqlist.txt  
 Output Set: N:\CRF3\08082001\I809638.raw

ENTERED

4 <110> APPLICANT: Mary Faris  
 5 Pia M. Challita-Eid  
 6 Steve Chappell Mitchell  
 7 Daniel E.H. Afar  
 8 Arthur B. Raitano  
 9 Aya Jakobovits  
 11 <120> TITLE OF INVENTION: 125P5C8: A TISSUE SPECIFIC PROTEIN  
 12 HIGHLY EXPRESSED IN VARIOUS CANCERS  
 15 <130> FILE REFERENCE: 129.35US01  
 17 <140> CURRENT APPLICATION NUMBER: 09/809,638  
 18 <141> CURRENT FILING DATE: 2001-03-14  
 20 <160> NUMBER OF SEQ ID NOS: 746  
 22 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 24 <210> SEQ ID NO: 1  
 25 <211> LENGTH: 2103  
 26 <212> TYPE: DNA  
 27 <213> ORGANISM: Homo sapiens  
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 31 ctctaccatg acctgggacc gatgatctat tactttctct tgcaaactc agaactcact 120  
 32 gggcttgaag gttttagtat agcatttctt tctccaatat tcttaacaat tactcctttc 180  
 33 tggaaattgg ttaacaagaa gtggatgcta accctgctga ggataatcac tattggcagc 240  
 34 atagcctcct tccaggctcc aaatgccaaa ctctgactga tggttcttgc gcttgggggtg 300  
 35 tcttctcctc tgatagtgc agetgtgact tgggtggctgg gaagtcattt gcaaagggtac 360  
 36 ctccagaattt ggggattcat tttaggacag attgttcttg ttgttctacg catatggtat 420  
 37 acttccactaa acccaatctg gagttatcag atgtccaaca aagtgatact gacattaagt 480  
 38 gccatagcca cacttgatcg tattggcaca gatggtgact gcagtaaacc tgaagaaaag 540  
 39 aagactgggtg aggtagccac ggggatggcc tctagacca actggctgct ggcaggggct 600  
 40 gcttttggtg gccttggtgt cctcaccac tgggtttttg gagaagtctc tcttggttcc 660  
 41 agatgggcag tgagtgggca tccacatcca gggccagatc ctaaccattt tggaggtgca 720  
 42 gtactgctgt gcttggcaag tggattgatg ctccatctt gtttgtgggt tctgtgtact 780  
 43 ggtttgatct ggtgggttac aggaacagct tcagctgctg ggtccttta cctgcacaca 840  
 44 tgggcagctg ctgtgtctgg ctgtgtcttc gccatcttta ctgcatccat gtggccccaa 900  
 45 acacttggac acctatttaa ctccagggaca aacctgggga aaaccatgac cattgccatg 960  
 46 atattttatc ttctagaaat atttttctgt gcctggtgca cagcttttaa gtttgtccca 1020  
 47 ggaggtgtct acgctagaga aagatcagat gtgcttttgg ggacaatgat gtttaattatc 1080  
 48 gggctgaata tgctatttgg tcttaagaaa aaccttgact tgcttcttca aacaaaaaac 1140  
 49 agttctaaag tgcttttcag aaagagtga aaatacatga aactttttct gtggctgctt 1200  
 50 gttggtgtgg gattgttggg attaggacta cggcataaag cctatgagag aaaactgggc 1260  
 51 aaagtggcac caaccaaaga ggtctctgct gccatctggc ctttcagggt tggatatgac 1320  
 52 aatgaagggt ggtctagtct agaaagatca gctcactgc tcaatgaaac aggtgcagat 1380  
 53 ttcataacaa ttttgagag tgatgcttct aagccctata tggggaacaa tgacttaacc 1440  
 54 atgtggctag gggaaaagtt gggtttctat acagactttg gtccaagcac aaggatatc 1500  
 55 acttggggga ttatggcttt gtcaagatac ccaattgtga aatctgagca tcaccttctt 1560  
 56 ccgtcaccag agggcgagat cgcaccagcc atcacattga ccgttaacat ttcgggcaag 1620  
 57 ctggttgatt ttgtcgtgac aacttttggg aaccacgaag atgacctga caggaaactg 1680  
 58 caggctattg ctgtttcaaa actactgaaa agtagctcta atcaagtgat atttctggga 1740

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59 tatatcactt cagcacctgg ctccagagat tatctacagc tcaactgaaca tggcaatgtg 1800
60 aaggatatcg acagcaactga tcatgacaga tgggtgtgaat acattatgta tcgagggctg 1860
61 atcaggttgg gttatgcaag aatctcccat gctgaactga gtgattcaga aattcagatg 1920
62 gcaaaattta ggatccctga tgaccccaact aattatagag acaaccagaa agtggtcata 1980
63 gaccacagag aagtttctga gaaaattcat tttaatccca gatttggatc ctacaaagaa 2040
64 ggacacaatt atgaaaacaa ccatcatttt catatgaata ctcccaaata ctttttatga 2100
65 aac 2103
67 <210> SEQ ID NO: 2
68 <211> LENGTH: 699
69 <212> TYPE: PRT
70 <213> ORGANISM: Homo sapiens
72 <400> SEQUENCE: 2
73 Met Thr Ser Leu Trp Arg Glu Ile Leu Leu Glu Ser Leu Leu Gly Cys
74 1 5 10 15
75 Val Ser Trp Ser Leu Tyr His Asp Leu Gly Pro Met Ile Tyr Tyr Phe
76 20 25 30
77 Pro Leu Gln Thr Leu Glu Leu Thr Gly Leu Glu Gly Phe Ser Ile Ala
78 35 40 45
79 Phe Leu Ser Pro Ile Phe Leu Thr Ile Thr Pro Phe Trp Lys Leu Val
80 50 55 60
81 Asn Lys Lys Trp Met Leu Thr Leu Leu Arg Ile Ile Thr Ile Gly Ser
82 65 70 75 80
83 Ile Ala Ser Phe Gln Ala Pro Asn Ala Lys Leu Arg Leu Met Val Leu
84 85 90 95
85 Ala Leu Gly Val Ser Ser Ser Leu Ile Val Gln Ala Val Thr Trp Trp
86 100 105 110
87 Ser Gly Ser His Leu Gln Arg Tyr Leu Arg Ile Trp Gly Phe Ile Leu
88 115 120 125
89 Gly Gln Ile Val Leu Val Val Leu Arg Ile Trp Tyr Thr Ser Leu Asn
90 130 135 140
91 Pro Ile Trp Ser Tyr Gln Met Ser Asn Lys Val Ile Leu Thr Leu Ser
92 145 150 155 160
93 Ala Ile Ala Thr Leu Asp Arg Ile Gly Thr Asp Gly Asp Cys Ser Lys
94 165 170 175
95 Pro Glu Glu Lys Lys Thr Gly Glu Val Ala Thr Gly Met Ala Ser Arg
96 180 185 190
97 Pro Asn Trp Leu Leu Ala Gly Ala Ala Phe Gly Ser Leu Val Phe Leu
98 195 200 205
99 Thr His Trp Val Phe Gly Glu Val Ser Leu Val Ser Arg Trp Ala Val
100 210 215 220
101 Ser Gly His Pro His Pro Gly Pro Asp Pro Asn Pro Phe Gly Gly Ala
102 225 230 235 240
103 Val Leu Leu Cys Leu Ala Ser Gly Leu Met Leu Pro Ser Cys Leu Trp
104 245 250 255
105 Phe Arg Gly Thr Gly Leu Ile Trp Trp Val Thr Gly Thr Ala Ser Ala
106 260 265 270
107 Ala Gly Leu Leu Tyr Leu His Thr Trp Ala Ala Ala Val Ser Gly Cys
108 275 280 285
109 Val Phe Ala Ile Phe Thr Ala Ser Met Trp Pro Gln Thr Leu Gly His

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110      290      295      300
111 Leu Ile Asn Ser Gly Thr Asn Pro Gly Lys Thr Met Thr Ile Ala Met
112 305      310      315      320
113 Ile Phe Tyr Leu Leu Glu Ile Phe Phe Cys Ala Trp Cys Thr Ala Phe
114      325      330      335
115 Lys Phe Val Pro Gly Gly Val Tyr Ala Arg Glu Arg Ser Asp Val Leu
116      340      345      350
117 Leu Gly Thr Met Met Leu Ile Ile Gly Leu Asn Met Leu Phe Gly Pro
118      355      360      365
119 Lys Lys Asn Leu Asp Leu Leu Leu Gln Thr Lys Asn Ser Ser Lys Val
120      370      375      380
121 Leu Phe Arg Lys Ser Glu Lys Tyr Met Lys Leu Phe Leu Trp Leu Leu
122 385      390      395      400
123 Val Gly Val Gly Leu Leu Gly Leu Gly Leu Arg His Lys Ala Tyr Glu
124      405      410      415
125 Arg Lys Leu Gly Lys Val Ala Pro Thr Lys Glu Val Ser Ala Ala Ile
126      420      425      430
127 Trp Pro Phe Arg Phe Gly Tyr Asp Asn Glu Gly Trp Ser Ser Leu Glu
128      435      440      445
129 Arg Ser Ala His Leu Leu Asn Glu Thr Gly Ala Asp Phe Ile Thr Ile
130      450      455      460
131 Leu Glu Ser Asp Ala Ser Lys Pro Tyr Met Gly Asn Asn Asp Leu Thr
132 465      470      475      480
133 Met Trp Leu Gly Glu Lys Leu Gly Phe Tyr Thr Asp Phe Gly Pro Ser
134      485      490      495
135 Thr Arg Tyr His Thr Trp Gly Ile Met Ala Leu Ser Arg Tyr Pro Ile
136      500      505      510
137 Val Lys Ser Glu His His Leu Leu Pro Ser Pro Glu Gly Glu Ile Ala
138      515      520      525
139 Pro Ala Ile Thr Leu Thr Val Asn Ile Ser Gly Lys Leu Val Asp Phe
140      530      535      540
141 Val Val Thr His Phe Gly Asn His Glu Asp Asp Leu Asp Arg Lys Leu
142 545      550      555      560
143 Gln Ala Ile Ala Val Ser Lys Leu Leu Lys Ser Ser Ser Asn Gln Val
144      565      570      575
145 Ile Phe Leu Gly Tyr Ile Thr Ser Ala Pro Gly Ser Arg Asp Tyr Leu
146      580      585      590
147 Gln Leu Thr Glu His Gly Asn Val Lys Asp Ile Asp Ser Thr Asp His
148      595      600      605
149 Asp Arg Trp Cys Glu Tyr Ile Met Tyr Arg Gly Leu Ile Arg Leu Gly
150      610      615      620
151 Tyr Ala Arg Ile Ser His Ala Glu Leu Ser Asp Ser Glu Ile Gln Met
152 625      630      635      640
153 Ala Lys Phe Arg Ile Pro Asp Asp Pro Thr Asn Tyr Arg Asp Asn Gln
154      645      650      655
155 Lys Val Val Ile Asp His Arg Glu Val Ser Glu Lys Ile His Phe Asn
156      660      665      670
157 Pro Arg Phe Gly Ser Tyr Lys Glu Gly His Asn Tyr Glu Asn Asn His
158      675      680      685

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159 His Phe His Met Asn Thr Pro Lys Tyr Phe Leu
160      690                      695
162 <210> SEQ ID NO: 3
163 <211> LENGTH: 287
164 <212> TYPE: DNA
165 <213> ORGANISM: Homo sapiens
167 <400> SEQUENCE: 3
168 gatcacgtgc tgcgatatac cttcacattg ccatgttcag tgagctgtag ataattctctg      60
169 gagccaggtg ctgaagtgat atatccaga aatatcactt gattagagct acttttcagt      120
170 agttttgaaa cagcaatagc ctgcagtttc ctgtcagagg catcttcgtg gttcccaaag      180
171 tgtgtcacga caaaatccac cagcttgccc gaaatgttaa cggccaatgt gatggctggt      240
172 gcgatcttgc tgtgttggcc aggctggtct caacgtgcag atagatc      287
174 <210> SEQ ID NO: 4
175 <211> LENGTH: 699
176 <212> TYPE: PRT
177 <213> ORGANISM: Homo sapiens
179 <400> SEQUENCE: 4
180 Met Thr Ser Leu Trp Arg Glu Ile Leu Leu Glu Ser Leu Leu Gly Cys
181 1      5      10      15
182 Val Ser Trp Ser Leu Tyr His Asp Leu Gly Pro Met Ile Tyr Tyr Phe
183      20      25      30
184 Pro Leu Gln Thr Leu Glu Leu Thr Gly Leu Glu Gly Phe Ser Ile Ala
185      35      40      45
186 Phe Leu Ser Pro Ile Phe Leu Thr Ile Thr Pro Phe Trp Lys Leu Val
187      50      55      60
188 Asn Lys Lys Trp Met Leu Thr Leu Leu Arg Ile Ile Thr Ile Gly Ser
189 65      70      75      80
190 Ile Ala Ser Phe Gln Ala Pro Asn Ala Lys Leu Arg Leu Met Val Leu
191      85      90      95
192 Ala Leu Gly Val Ser Ser Ser Leu Ile Val Gln Ala Val Thr Trp Trp
193      100     105     110
194 Ser Gly Ser His Leu Gln Arg Tyr Leu Arg Ile Trp Gly Phe Ile Leu
195      115     120     125
196 Gly Gln Ile Val Leu Val Val Leu Arg Ile Trp Tyr Thr Ser Leu Asn
197      130     135     140
198 Pro Ile Trp Ser Tyr Gln Met Ser Asn Lys Val Ile Leu Thr Leu Ser
199 145     150     155     160
200 Ala Ile Ala Thr Leu Asp Arg Ile Gly Thr Asp Gly Asp Cys Ser Lys
201      165     170     175
202 Pro Glu Glu Lys Lys Thr Gly Glu Val Ala Thr Gly Met Ala Ser Arg
203      180     185     190
204 Pro Asn Trp Leu Leu Ala Gly Ala Ala Phe Gly Ser Leu Val Phe Leu
205      195     200     205
206 Thr His Trp Val Phe Gly Glu Val Ser Leu Val Ser Arg Trp Ala Val
207      210     215     220
208 Ser Gly His Pro His Pro Gly Pro Asp Pro Asn Pro Phe Gly Gly Ala
209 225     230     235     240
210 Val Leu Leu Cys Leu Ala Ser Gly Leu Met Leu Pro Ser Cys Leu Trp
211      245     250     255

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```

212 Phe Arg Gly Thr Gly Leu Ile Trp Trp Val Thr Gly Thr Ala Ser Ala
213                               260                               265                               270
214 Ala Gly Leu Leu Tyr Leu His Thr Trp Ala Ala Ala Val Ser Gly Cys
215                               275                               280                               285
216 Val Phe Ala Ile Phe Thr Ala Ser Met Trp Pro Gln Thr Leu Gly His
217                               290                               295                               300
218 Leu Ile Asn Ser Gly Thr Asn Pro Gly Lys Thr Met Thr Ile Ala Met
219 305                               310                               315                               320
220 Ile Phe Tyr Leu Leu Glu Ile Phe Phe Cys Ala Trp Cys Thr Ala Phe
221                               325                               330                               335
222 Lys Phe Val Pro Gly Gly Val Tyr Ala Arg Glu Arg Ser Asp Val Leu
223                               340                               345                               350
224 Leu Gly Thr Met Met Leu Ile Ile Gly Leu Asn Met Leu Phe Gly Pro
225                               355                               360                               365
226 Lys Lys Asn Leu Asp Leu Leu Leu Gln Thr Lys Asn Ser Ser Lys Val
227                               370                               375                               380
228 Leu Phe Arg Lys Ser Glu Lys Tyr Met Lys Leu Phe Leu Trp Leu Leu
229 385                               390                               395                               400
230 Val Gly Val Gly Leu Leu Gly Leu Gly Leu Arg His Lys Ala Tyr Glu
231                               405                               410                               415
232 Arg Lys Leu Gly Lys Val Ala Pro Thr Lys Glu Val Ser Ala Ala Ile
233                               420                               425                               430
234 Trp Pro Phe Arg Phe Gly Tyr Asp Asn Glu Gly Trp Ser Ser Leu Glu
235                               435                               440                               445
236 Arg Ser Ala His Leu Leu Asn Glu Thr Gly Ala Asp Phe Ile Thr Ile
237                               450                               455                               460
238 Leu Glu Ser Asp Ala Ser Lys Pro Tyr Met Gly Asn Asn Asp Leu Thr
239 465                               470                               475                               480
240 Met Trp Leu Gly Glu Lys Leu Gly Phe Tyr Thr Asp Phe Gly Pro Ser
241                               485                               490                               495
242 Thr Arg Tyr His Thr Trp Gly Ile Met Ala Leu Ser Arg Tyr Pro Ile
243                               500                               505                               510
244 Val Lys Ser Glu His His Leu Leu Pro Ser Pro Glu Gly Glu Ile Ala
245                               515                               520                               525
246 Pro Ala Ile Thr Leu Thr Val Asn Ile Ser Gly Lys Leu Val Asp Phe
247                               530                               535                               540
248 Val Val Thr His Phe Gly Asn His Glu Asp Asp Leu Asp Arg Lys Leu
249 545                               550                               555                               560
250 Gln Ala Ile Ala Val Ser Lys Leu Leu Lys Ser Ser Ser Asn Gln Val
251                               565                               570                               575
252 Ile Phe Leu Gly Tyr Ile Thr Ser Ala Pro Gly Ser Arg Asp Tyr Leu
253                               580                               585                               590
254 Gln Leu Thr Glu His Gly Asn Val Lys Asp Ile Asp Ser Thr Asp His
255                               595                               600                               605
256 Asp Arg Trp Cys Glu Tyr Ile Met Tyr Arg Gly Leu Ile Arg Leu Gly
257                               610                               615                               620
258 Tyr Ala Arg Ile Ser His Ala Glu Leu Ser Asp Ser Glu Ile Gln Met
259 625                               630                               635                               640
260 Ala Lys Phe Arg Ile Pro Asp Asp Pro Thr Asn Tyr Arg Asp Asn Gln

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VERIFICATION SUMMARY

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